

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 24, 2003, 16:07:11 ; Search time 36 Seconds

(without alignments)  
1493.842 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 261

Sequence: 1 MGLSPRRKSLPSLSVSSV.....RESLSFYISLNDKAVSLDDA 261

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

- 1: SP archaea:\*
- 2: SP bacteria:\*
- 3: SP fungi:\*
- 4: SP human:\*
- 5: SP invertebrate:\*
- 6: SP mammal:\*
- 7: SP mnc:\*
- 8: SP organelle:\*
- 9: SP phage:\*
- 10: SP plant:\*
- 11: SP rodent:\*
- 12: SP virus:\*
- 13: SP vertebrate:\*
- 14: SP unclassified:\*
- 15: SP tvirus:\*
- 16: SP bacteriophage:\*
- 17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	100.0	261	4 Q9H6Q3	Q9H6Q3 homo sapien
2	197	75.5	197	4 Q9H135	Q9H135 homo sapien
3	178	68.2	210	4 Q9H718	Q9H718 homo sapien
4	63	24.1	63	4 Q96Q14	Q96Q14 homo sapien
5	37	14.2	179	11 Q9D129	Q9D129 mus musculu
6	37	14.2	259	11 Q8V142	Q8V142 mus musculu
7	37	14.2	259	11 Q8R4L0	Q8R4L0 mus musculu
8	9	3.4	423	4 Q8TDS5	Q8TDS5 mus musculu
9	9	3.4	505	4 Q961N1	Q961N1 mus musculu
10	8	3.1	64	4 Q8TCL7	Q8TCL7 mus sapien
11	8	3.1	93	6 Q9T0B7	Q9T0B7 mus sapien
12	8	3.1	135	4 Q9V779	Q9V779 mus sapien
13	8	3.1	138	12 Q8V4S2	Q8V4S2 mus sapien
14	8	3.1	161	4 Q9H817	Q9H817 mus sapien
15	8	3.1	177	4 P78453	P78453 mus sapien
16	8	3.1	178	16 Q98KH4	Q98KH4 rhizobium

17	8	3.1	217	11 Q9CX99	Q9CX99 mus musculu
18	8	3.1	217	13 Q9PU11	Q9PU11 xenopus lae
19	8	3.1	258	5 Q9I7U9	Q9I7U9 dirosophila
20	8	3.1	276	4 Q13239	Q13239 homo sapien
21	8	3.1	280	11 Q8QZX8	Q8QZX8 mus musculu
22	8	3.1	281	11 Q60898	Q60898 mus musculu
23	8	3.1	447	5 Q94262	Q94262 caenorhabdi
24	8	3.1	461	11 Q63789	Q63789 rattus norv
25	8	3.1	467	5 Q77132	Q77132 hydra atten
26	8	3.1	488	13 Q13064	Q13064 xenopus lae
27	8	3.1	499	10 Q94AV6	Q94AV6 arabidopsis
28	8	3.1	502	13 Q9DDK6	Q9DDK6 salmo salar
29	8	3.1	506	11 Q62662	Q62662 rattus norv
30	8	3.1	512	11 Q61364	Q61364 mus musculu
31	8	3.1	512	11 Q61745	Q61745 mus musculu
32	8	3.1	512	11 Q922K9	Q922K9 mus musculu
33	8	3.1	517	11 Q63206	Q63206 rattus norv
34	8	3.1	697	3 Q8WZ3	Q8WZ3 neotospora
35	8	3.1	743	3 P87122	P87122 schizosacch
36	8	3.1	810	10 Q9FFK6	Q9FFK6 arabidopsis
37	8	3.1	827	5 Q9BL20	Q9BL20 caenorhabdi
38	7	2.7	17	4 Q9GZT7	Q9GZT7 homo sapien
39	7	2.7	40	4 Q9HCR6	Q9HCR6 homo sapien
40	7	2.7	61	4 Q9HCR7	Q9HCR7 homo sapien
41	7	2.7	70	10 Q9LUN9	Q9LUN9 pyrus pyrif
42	7	2.7	93	13 Q9PSU0	Q9PSU0 brachydanio
43	7	2.7	96	10 Q9C7L8	Q9C7L8 arabidopsis
44	7	2.7	102	4 Q8WUD9	Q8WUD9 homo sapien
45	7	2.7	106	16 Q55970	Q55970 synecocyst
46	7	2.7	109	11 Q9DAU0	Q9DAU0 mus musculu
47	7	2.7	114	16 Q9S572	Q9S572 pseudomonas
48	7	2.7	115	16 Q8V8W4	Q8V8W4 listeria mo
49	7	2.7	117	4 Q9URU7	Q9URU7 homo sapien
50	7	2.7	118	16 Q92FH6	Q92FH6 listeria in
51	7	2.7	127	5 Q9NLP4	Q9NLP4 leishmania
52	7	2.7	128	11 Q9D980	Q9D980 mus musculu
53	7	2.7	136	16 Q9PFA8	Q9PFA8 xyloella fas
54	7	2.7	140	16 Q8UH38	Q8UH38 agrobacteri
55	7	2.7	154	12 Q65956	Q65956 hepatitis b
56	7	2.7	172	10 Q94H56	Q94H56 oryza sativ
57	7	2.7	177	4 Q8WMB3	Q8WMB3 homo sapien
58	7	2.7	179	10 Q9AS32	Q9AS32 oryza sativ
59	7	2.7	180	16 Q915V4	Q915V4 pseudomonas
60	7	2.7	181	4 Q9HCR8	Q9HCR8 homo sapien
61	7	2.7	188	16 Q92V87	Q92V87 rhizobium m
62	7	2.7	189	10 Q9CSZ4	Q9CSZ4 arabidopsis
63	7	2.7	189	10 Q9SCS9	Q9SCS9 mus musculu
64	7	2.7	190	10 Q8K144	Q8K144 solanum tub
65	7	2.7	192	17 Q8ZV47	Q8ZV47 pyrobaculum
66	7	2.7	193	17 Q9V2U6	Q9V2U6 pyrococcus
67	7	2.7	198	5 Q9U4D4	Q9U4D4 caenorhabdi
68	7	2.7	200	11 Q9D387	Q9D387 mus musculu
69	7	2.7	200	16 Q84606	Q84606 chlamydia t
70	7	2.7	201	2 Q87962	Q87962 streptomyce
71	7	2.7	202	16 Q9PUD9	Q9PUD9 chlamydia m
72	7	2.7	206	4 Q9P0N6	Q9P0N6 homo sapien
73	7	2.7	217	16 Q8XB62	Q8XB62 escherichia
74	7	2.7	219	10 Q9Y0P6	Q9Y0P6 thalassiosi
75	7	2.7	219	16 Q9CUI3	Q9CUI3 lactococcus
76	7	2.7	224	11 Q9DC70	Q9DC70 mus musculu
77	7	2.7	227	8 Q9WEC3	Q9WEC3 pythium ult
78	7	2.7	234	10 Q8W320	Q8W320 oryza sativ
79	7	2.7	237	10 Q9LKG0	Q9LKG0 lycopersico
80	7	2.7	245	16 Q9RVU9	Q9RVU9 mus musculu
81	7	2.7	248	16 Q8URF9	Q8URF9 deinococcus
82	7	2.7	251	10 Q8S241	Q8S241 agrobacteri
83	7	2.7	257	10 Q9LRL6	Q9LRL6 arabidopsis
84	7	2.7	257	11 Q9DAP6	Q9DAP6 mus musculu
85	7	2.7	262	17 Q8TKL4	Q8TKL4 methanosaer
86	7	2.7	267	10 Q9SXP8	Q9SXP8 arabidopsis
87	7	2.7	269	16 Q92W32	Q92W32 rhizobium m
88	7	2.7	270	10 Q94ZP5	Q94ZP5 oryza sativ
89	7	2.7	273	10 Q9SQU4	Q9SQU4 brassica ca

90	7	2.7	275	16	Q99U25	Q99U25 staphylococ
91	7	2.7	276	2	Q8RX90	Q8RX90 micrococcus
92	7	2.7	278	2	Q53603	Q53603 streptomyces
93	7	2.7	278	16	Q50890	Q50890 borrelia bu
94	7	2.7	278	16	Q99YU6	Q99YU6 dinococcus
95	7	2.7	278	16	Q50889	Q50889 borrelia bu
96	7	2.7	284	3	Q6156	Q6156 schistosom
97	7	2.7	287	16	Q9PKP4	Q9PKP4 chlamydia m
98	7	2.7	293	4	Q9BOE7	Q9BOE7 homo sapien
99	7	2.7	294	16	Q9KXK1	Q9KXK1 vibrio chol
100	7	2.7	294	16	Q9PNF4	Q9PNF4 campylobact

## ALIGNMENTS

## RESULT 1

Q9H6Q3 PRELIMINARY; PRT; 261 AA.

AC Q9H6Q3: 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE CDNA: FJ221992 fig, clone HEP6554 (Src-like adapter protein-2)  
 DE (Modulator of antigen receptor signaling MARS).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kawabata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Oka T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,  
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,  
 RT "MEDO human cDNA sequencing project."  
 RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21553259; PubMed=1196592;  
 RA Holland S.J., Liao X.C., Mendenhall M.K., Zhou X., Pardo J., Chu P.,  
 RA Spencer C., Fu A.C., Sheng N., Yu P., Pail E., Nagin A., Shen M.,  
 RA Yu S., Chan E., Wu X., Li C., Wolsechslager M., Aversa G.,  
 RA Kolbinger F., Bennett M.K., Molinaux S., Luo Y., Payan D.G.,  
 RA Mancebo H.S.Y., Wu J.,  
 RT "Functional cloning of src-like adapter protein-2 (SLAP-2), a novel  
 RT inhibitor of antigen receptor signaling."  
 RL J. Exp. Med. 194.1263-1276(2001).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RA Loreto M.P., McGlade C.J.,  
 RT "Modulator of Antigen Receptor Signaling (MARS)."  
 RL Submitted (Jul-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL: AK025645; BA15201.1;  
 DR EMBL: AF326353; AAL29204.1;  
 DR EMBL: AF290985; AAL38197.1;  
 DR HSP: P06239; ILKK.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH3; 1.  
 DR PRINTS: PR00401; SH2DOMAIN.  
 DR PRODOM: PD00093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR PROSITE: PS00001; SH2; 1.  
 DR PROSITE: PS00002; SH3; 1.  
 KW SH3 domain; Receptor.  
 SQ SEQUENCE 261 AA; 26585 MW; 858AF03451672B3D CRC64;

Query Match 100.0%; Score 261; DB 4; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1,76-254;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MGSLPSRRKSLPSPISSSSVGGPGVTMEAKSKATAVALLSPAGPAPSLRIGELT 60
Db	1 MGSLPSRRKSLPSPISSSSVGGPGVTMEAKSKATAVALLSPAGPAPSLRIGELT 60
Qy	61 IVSEGDGMVTVSEVSGREYNIPSVHAKVSHQWYEGLSREKAEELLLPGNPGAFI 120
Db	61 IVSEGDGMVTVSEVSGREYNIPSVHAKVSHQWYEGLSREKAEELLLPGNPGAFI 120
Qy	121 RESQTRRSYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLA 180
Db	121 RESQTRRSYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLA 180
Qy	181 DDICCLKEPCVLRAGPLPGKDIPLVTYQRTPLNMEELDSLLFSEATGEESLSEG 240
Db	181 DDICCLKEPCVLRAGPLPGKDIPLVTYQRTPLNMEELDSLLFSEATGEESLSEG 240
Qy	241 LRESISFYISLNDVAVSLDDA 261
Db	241 LRESISFYISLNDVAVSLDDA 261

## RESULT 2

Q9H135 PRELIMINARY; PRT; 197 AA.

AC Q9H135: 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE D1977B1.1 (Novel protein tyrosine kinase with Src homology domain 2  
 DE (SH2) domain) (Fragment).  
 GN D1977B1.1  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lloyd D.,  
 RL Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AL050318; CAB75365.1;  
 DR HSP: P06239; ILKK.  
 DR InterPro: IPR000980; SH2.  
 DR Pfam: PF00017; SH2; 1.  
 DR PRINTS: PR00401; SH2DOMAIN.  
 DR PRODOM: PD00093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR PROSITE: PS00001; SH2; 1.  
 KW Kinase.  
 FT NON-TER  
 SQ SEQUENCE 197 AA; 22124 MW; EF01FE7A85C5C1F1 CRC64;

Query Match 75.5%; Score 197; DB 4; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4,2e-190;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	65 DDDMTTVLSEVSGREYNIPSVHAKVSHQWYEGLSREKAEELLLPGNPGAFI 124
Db	1 DDDMTTVLSEVSGREYNIPSVHAKVSHQWYEGLSREKAEELLLPGNPGAFI 124
Qy	125 TRRGYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLADIC 184
Db	61 TRRGYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLADIC 120
Qy	185 CLIKPCVLRAGPLPGKDIPLVTYQRTPLNMEELDSLLFSEATGEESLSEG 244
Db	121 CLIKPCVLRAGPLPGKDIPLVTYQRTPLNMEELDSLLFSEATGEESLSEG 180
Qy	245 LSFYISLNDVAVSLDDA 261
Db	181 LSFYISLNDVAVSLDDA 197

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RESULT 3
Q8WY18 PRELIMINARY; PRT; 210 AA.
AC Q8WY18;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Modulator of antigen receptor signaling, putative splice isoform
DE MARS-V.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Loreto M.P., McGlade C.J.;
RT "Modulator of Antigen Receptor Signaling (MARS) - putative splice
variant.",
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF290986; AAL38198.1; -.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KM Receptor.
SQ SEQUENCE 210 AA, 23103 MW, BED62208E53A472E CRC64;

Query Match 68.2%; Score 178; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 6.2e-171;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLPSRRKSLPSPLSSVGGQGVPTMEARSKATVAALGSPAGPABLSLRGEPLT 60
DB 1 MGSLPSRRKSLPSPLSSVGGQGVPTMEARSKATVAALGSPAGPABLSLRGEPLT 60

QY 61 IVSEDDGMWTVLSEVSGREYIPSVYVAKVSHGWLVEGLSREKAEELLILPGPGAFIL 120
DB 61 IVSEDDGMWTVLSEVSGREYIPSVYVAKVSHGWLVEGLSREKAEELLILPGPGAFIL 120

QY 121 RRSQTRRGSGYSLSVRLSRPASMDRIHRHRIHCDNGLYISPLTTPPSLQALVDHYSE 178
DB 121 RRSQTRRGSGYSLSVRLSRPASMDRIHRHRIHCDNGLYISPLTTPPSLQALVDHYSE 178

RESULT 4
Q96Q14 PRELIMINARY; PRT; 63 AA.
AC Q96Q14;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE DJ460J8.2 (Novel protein tyrosine kinase with Src homology 2 (SH2)
DE domain.) (Fragment).
DE domain.
GN DJ97781.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Skuce C.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031662; CAC44645.1; -.
KM Kinase.

FT NON TER 63 63
SQ SEQUENCE 63 AA; 6350 MW; 3EC599C9F1723053 CRC64;

Query Match 24.1%; Score 63; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.7e-55;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLPSRRKSLPSPLSSVGGQGVPTMEARSKATVAALGSPAGPABLSLRGEPLT 60
DB 1 MGSLPSRRKSLPSPLSSVGGQGVPTMEARSKATVAALGSPAGPABLSLRGEPLT 60

QY 61 IVS 63
DB 61 IVS 63

RESULT 5
Q9D129 PRELIMINARY; PRT; 179 AA.
AC Q9D129;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE A930009E21R1K protein.
GN A930009E21R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=RETINA;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Cavaant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Stanbaj F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baret G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.U., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshewski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.",
RL Nature 409:685-690(2001).
DR EMBL; AK020837; BAB32223.1; -.
DR HSSP; P06239; ILKK.
DR MGP; MGI:1925049; A930009E21R1K.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00017; SH2; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 179 AA; 19926 MW; 60477A0CF4003FCD CRC64;

Query Match 14.2%; Score 37; DB 11; Length 179;
Best Local Similarity 100.0%; Pred. No. 6.9e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 HGMWLEGLSREKAEELLILPGPGAFILRESQTRRG 128
DB 11 HGMWLEGLSREKAEELLILPGPGAFILRESQTRRG 47

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QY 165 TFPGLQALV 173  
 |||||  
 DB 194 TFPGLQALV 202

## RESULT 10

08TC17 PRELIMINARY; PRT; 64 AA.  
 ID 08TC17  
 AC 08TC17  
 DT 01-JUN-2002 (TEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)  
 DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG;  
 RA Strauberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC026233; AAH26233.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 64 AA; 7183 MW; 0D8C6FF43E221DC CRC64;

Query Match 3.1%; Score 8; DB 4; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRS 123  
 |||||  
 DB 29 GAFLIRS 36

## RESULT 11

09TUB7 PRELIMINARY; PRT; 93 AA.  
 ID 09TUB7  
 AC 09TUB7  
 DT 01-MAY-2000 (TEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)  
 DE Growth factor receptor-bound protein 2 (Fragment).  
 OS Ursus maritimus (Polar bear) (Thalarcos maritimus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
 NCBI\_TaxID=29073;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Libertes D.A., Schreiber D.R., Chamberlin S.G., Govindarajan S.,  
 RA Thomson J.M., Wigger M., Benner S.A.;  
 RT "Evolutionary Analysis of the Src Homology 2 (SH2) Domain";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF093133; AAF0915.1; -.  
 DR HSSP: P29354; 1BMB.  
 DR InterPro: IPR000980; SH2.  
 DR Pfam: PF00017; SH2; 1.  
 DR PRINTS: PR00401; SH2DOMAIN.  
 DR ProDom: PD000093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR PROSITE: PSS0001; SH2; 1.  
 KW Receptor.  
 FT NON TER 1  
 FT NON TER 93  
 SQ SEQUENCE 93 AA; 10837 MW; 3546DCC1E1A1F3A CRC64;

Query Match 3.1%; Score 8; DB 6; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRS 123

DB 22 GAFLIRS 29  
 |||||

## RESULT 12

099779 PRELIMINARY; PRT; 135 AA.  
 ID 099779  
 AC 099779  
 DT 01-MAY-1997 (TEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)  
 DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE Hypothetical 14.4 kDa protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=96207227; PubMed=8619474;  
 RA Anderson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;  
 RT "A 'double adaptor' method for improved shotgun library  
 construction";  
 RL Anal. Biochem. 236:107-113 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=97264341; PubMed=9110174;  
 RA Yu W., Andersson B., Morley K.C., Muzny D.M., Ding Y., Liu W.,  
 RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;  
 RT "Large-scale concatenation cDNA sequencing";  
 RL Genome Res. 7:353-358 (1997).  
 DR EMBL: U79280; AAB50218.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 135 AA; 14406 MW; D4B7C08054BF41C7 CRC64;

Query Match 3.1%; Score 8; DB 4; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AVAGSFP 44  
 |||||  
 DB 101 AVAGSFP 108

## RESULT 13

08VAS2 PRELIMINARY; PRT; 138 AA.  
 ID 08VAS2  
 AC 08VAS2  
 DT 01-MAR-2002 (TEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)  
 DE Wav320 (WSSV376).  
 OS White spot syndrome virus (WSSV).  
 OC Viruses; unclassified viruses.  
 NCBI\_TaxID=92652;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21548311; PubMed=11689662;  
 RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;  
 RT "Complete genome sequence of the shrimp white spot bacilliform  
 virus";  
 RL J. Virol. 75:11811-11820 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TAIWAN;  
 RX MEDLINE=20517548; PubMed=11062040;  
 RA Tsai M.F., Yu H.T., Tzeng H.F., Liu J.H., Chou C.M., Huang C.J.,

RA Mang C.H., Lin J.Y., Kou G.H., Lo C.F.;  
 RT "Identification and characterization of a shrimp white spot syndrome  
 RT virus (WSSV) gene that encodes a novel chimeric polypeptide of  
 RT cellular-type thymidine kinase and thymidylate kinase."  
 RL Virology 277:100-110(2000).

RN [4]  
 RP SEQUENCE FROM N.A.

RC STRAIN=TAIWAN;

RA MEDLINE=21844071; PubMed=11853398;

RA Chen L.L., Liu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,

RA Lo C.F., Kou G.H.;

RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white  
 RT spot syndrome virus and characterization of the motif important for  
 RT targeting VP35 to the nuclei of transfected insect cells."  
 RL Virology 293:44-53(2002).

RN [5]  
 RP SEQUENCE FROM N.A.

RC STRAIN=TAIWAN;

RA Lo C.-F., Kou G.-H.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RA EMBL: AF332093; AF33322.1; -

DR EMBL: AF440570; AAL89244.1; -

SO SEQUENCE 138 AA; 13970 MW; 8A3ABC08D8E804B CRC64;

Query Match 3.1%; Score 8; DB 12; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 9.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PSPSLSS 19  
 |||||

DB 58 PSPSLSS 65

RESULT 14

Q9HB17 PRELIMINARY; PRT; 161 AA.

AC Q9HB17; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Ste-like adapter protein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]  
 RP SEQUENCE FROM N.A.

RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,

RA Jorje, Rd, Schlindner M.B., Menzel U., Dettle M.D., Baumgart C.,

RA Jahn N., Rosenthal A.;

RT "Chromosome 8 genomic sequence."

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.

RA Genome Sequencing Center Jena;

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

DR EMBL: AF235100; AAG29878.1; -

DR HSSP: P08631; 3HCK.

DR InterPro: IPR000980; SH2.

DR InterPro: IPR001452; SH3.

DR Pfam: PF00017; SH2; 1.

DR Pfam: PF00018; SH3; 1.

DR PRINTS: PR00401; SH2DOMAIN.

DR PRODOM: PD000093; SH2; 1.

DR SMART: SM00252; SH2; 1.

DR SMART: SM00326; SH3; 1.

DR PROSITE: PS50001; SH2; 1.

DR PROSITE: PS50002; SH3; 1.

DR SH3 domain.

KW NON TER 161

FT SEQUENCE 161 AA; 18493 MW; FC28546604E5B20 CRC64;

Query Match 3.1%; Score 8; DB 4; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 YISPRITF 166  
 |||||

DB 143 YISPRITF 150

RESULT 15

P78453 PRELIMINARY; PRT; 177 AA.

AC P78453;

DT 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Tyrosine kinase (FGR proto-oncogene encoded p55-C-FGR protein)

OS (Fragment).

GN C-FGR.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]  
 RP SEQUENCE FROM N.A.

RA MEDLINE=89134667; PubMed=2852026;

RA Brickell P.M., Patel M.;

RT "Structure and expression of c-fgr protooncogene mRNA in Epstein-Barr

RT virus converted cell lines."

RL Br. J. Cancer 58:704-709(1988).

RN [2]  
 RP SEQUENCE OF 46-85 FROM N.A.

RA MEDLINE=88094395; PubMed=3275868;

RA Kalamine S., Nocard V., Rao C.D., Miki T., Cheah M.S., Tronick S.R.,

RA Robbins K.C.;

RT "Primary structure of the human fgr proto-oncogene product p55c-fgr."

RL Mol. Cell. Biol. 8:259-266(1988).

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

DR EMBL: M27454; AA33679.1; -

DR EMBL: M19721; AA52452.1; -

DR HSSP: P06241; 1AOU.

DR InterPro: IPR000980; SH2.

DR InterPro: IPR001452; SH3.

DR Pfam: PF00017; SH2; 1.

DR Pfam: PF00018; SH3; 1.

DR PRINTS: PR00401; SH2DOMAIN.

DR PRINTS: PR00452; SH3DOMAIN.

DR PRODOM: PD000066; SH3; 1.

DR PRODOM: PD000093; SH2; 1.

DR SMART: SM00326; SH3; 1.

DR PROSITE: PS50001; SH2; 1.

DR PROSITE: PS50002; SH3; 1.

DR SH3 domain.

KW NON TER 177

FT SEQUENCE 177 AA; 19354 MW; 11ACD73BAF343B CRC64;

Query Match 3.1%; Score 8; DB 4; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRS 123  
 |||||

DB 166 GAFLIRS 173

RESULT 16

Q98KH4 PRELIMINARY; PRT; 178 AA.

AC Q98KH4; 01-OCT-2001 (TREMBlrel. 18, Created)

DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Hypothetical protein mlti474.

GN MMR1474.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_taxid=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAF03099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Saito S.,  
 RA Watanabe A., Ideasa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuo A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti."  
 RL DNA Ref. 7:331-338 (2000).  
 DR EMBL; AF002997; BAB6840.1.-.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 178 AA; 19823 MW; EB4B7DEB9D36D46 CRC64;  
 Query Match 3.1%; Score 8; DB 16; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 57 EPTIVSE 64  
 DB 133 EPTIVSE 140  
 RESULT 17  
 O9CX99 PRELIMINARY; PRT; 217 AA.  
 AC O9CX99.  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE 8430435N19Rik protein.  
 GN GRAP OR 8430435N19Rik.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LUNG;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Moncada P.,  
 RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Williams L.,  
 RA Wynnaw-Borle A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.  
 DR EMBL; AK018457; BAB31222.1.-.  
 DR HSSP; P29354; 1BM2.  
 DR MGD; MGI:1918770; Grap.  
 DR InterPro; IPR00108; Neu\_cyt\_fact\_2.  
 DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR Pfam; PF00499; P67PHOX.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRODOM; PD000066; SH3; 2.  
 DR PRODOM; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 DR SH3 domain.  
 SQ SEQUENCE 217 AA; 25277 MW; 1AF124C3D2773DD2 CRC64;  
 Query Match 3.1%; Score 8; DB 11; Length 217;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 116 GAFLIRS 123  
 DB 81 GAFLIRS 88  
 RESULT 18  
 O9PUI1 PRELIMINARY; PRT; 217 AA.  
 AC O9PUI1.  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Grb2 protein.  
 GN GRB2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_taxid=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gollaset C., Shi D.L., Boucancut J.C.;  
 RT "Selective inhibition of neural induction but not mesoderm induction  
 RT by interfering mutants of *Sem-5/Grb2*."  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.  
 DR EMBL; AJ223061; CAB59279.1.-.  
 DR HSSP; P29354; 1GHU.  
 DR InterPro; IPR000108; Neu\_cyt\_fact\_2.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR PRINTS; PR00499; P67PHOX.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRODOM; PD000066; SH3; 2.  
 DR PRODOM; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 DR SH3 domain.  
 SQ SEQUENCE 217 AA; 25335 MW; 2349A68260F9D4CD CRC64;  
 Query Match 3.1%; Score 8; DB 13; Length 217;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 116 GAFLIRS 123  
 DB 81 GAFLIRS 88

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RESULT 19
Q91709 PRELIMINARY; PRT; 258 AA.
AC Q91709;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CG16778 protein.
GN CG16778.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pserygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyridae; Drosophilidae; Drosophila.
OK NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Planckoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrara S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.R., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kratz C., Kravitz S., Kulp D., Lai Z.,
RA Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pauley J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003466; AAG2201.1; -
DR FLYBase; FBgn035093; CG16778.
SQ SEQUENCE 258 AA; 28886 MW; 4BD0181BF414FB2 CRC64;

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Query Match 3.1%; Score 8; DB 5; Length 258;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 13 SPSSSSV 20
DB 219 SPSSSSV 226

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RESULT 20
Q13239 PRELIMINARY; PRT; 276 AA.
AC Q13239;

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DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative SRC-like adapter protein (SLAP) (SRC-like-adapter).
GN SLAP.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96423054; PubMed=8825655;
RX Angillet M., Wells D.E., Chakravarti A., Pandey A.;
RA "Chromosomal localization of the mouse Src-like adapter protein (Slap)
RT gene and its putative human homolog SLA."
RL Genomics 30:623-625(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRNIN;
RA Mijerink P.H.S., Zorn G., Binker H., Bolhuis P.A., Baas F.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Otsuki T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Kalaydjieva L., Goodman R., Greham D., Baas F.,
RA Unger, R., Schinabel M., Wen G., Menzel U., Dettle M., Baumgart C.,
RA Rosenthal A.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC - - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; U30473; AAC50357.1; -
DR EMBL; U44403; AAC27662.1; -
DR EMBL; D89077; BA13758.1; -
DR EMBL; AF305872; AAG17933.1; -
DR EMBL; BC007042; AA07042.1; -
DR HSSP; P08631; 3HCK.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00017; SH2_1.
DR Pfam; PF00018; SH3_1.
DR PRINTS; PR00401; SH3DOMAIN.
DR PRODOM; PD000093; SH2_1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR SH3 domain. 276 AA; 31156 MW; B0FC07D7B2ECA378 CRC64;
SQ

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Query Match 3.1%; Score 8; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 159 YISPLRTP 166
DB 143 YISPLRTP 150

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RESULT 21
Q8QZX8 PRELIMINARY; PRT; 280 AA.
ID Q8QZX8
AC Q8QZX8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

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DE Src-like adapter protein SLAP (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ILS, AND ISS;  
 RX MEDLINE=21363810; PubMed=11471062;  
 RA Ehlinger M.A., Thompson J., Conroy O., Xu Y., Yang F., Camille J.,  
 Beeson M., Gordon L., Bennett B., Johnson T.E., Sikeia J.M.,  
 RT "High-throughput sequence identification of gene coding variants  
 within alcohol-related QTLs."  
 RL Mamm. Genome 12:657-663(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ILS, AND ISS;  
 RA Ehlinger M.A., Thompson J., Conroy O., Xu Y., Yang F., Camille J.,  
 Beeson M., Gordon L., Bennett B., Johnson T.E., Sikeia J.M.,  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY079449; AAL87537.1; -  
 DR EMBL; AY079450; AAL87538.1; -  
 FT NON TER 1  
 FT NON TER 280  
 SO SEQUENCE 280 AA; 31549 MW; A05G3BF7EAD951 CRC64;  
 Query Match 3.1%; Score 8; DB 11; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 159 YISPRLTF 166  
 Db 142 YISPRLTF 149  
 RESULT 22  
 ID Q60898 PRELIMINARY; PRT; 281 AA.  
 AC Q60898;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)  
 DE SRC-like adapter protein.  
 GN SLA OR SLAP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=95370243; PubMed=7543898;  
 RA Pandey A., Duan H., Dixit V.M.,  
 RT "Characterization of a novel Src-like adapter protein that associates  
 with the ECK receptor tyrosine kinase."  
 RL J. Biol. Chem. 270:19201-19204(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20093985; PubMed=10630289;  
 RA Carrier A., Nguyen C., Victorero G., Granjeand S., Rocha D.,  
 RA Bernard K., Mizek A., Ferrer P., Walissen M., Naquet P.,  
 RA Walissen B., Jordan B.,  
 RT "Differential gene expression in CD3e- and RAG1-deficient thymuses:  
 RT definition of a set of genes potentially involved in thymocyte  
 RT maturation."  
 RL Immunogenetics 50:255-270(1999).  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL; U29056; AAB2756.1; -  
 DR EMBL; AJ131777; CAB6139.1; -  
 DR HSSP; P16277; 1BLK  
 DR MGD; MGI:104293; SLA.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PD00401; SH3DOMAIN.  
 DR PRODOM; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW SH3 domain.  
 SQ SEQUENCE 281 AA; 31680 MW; 8347921656A74DA1 CRC64;  
 Query Match 3.1%; Score 8; DB 11; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 159 YISPRLTF 166  
 Db 143 YISPRLTF 150  
 RESULT 23  
 ID Q94262 PRELIMINARY; PRT; 447 AA.  
 AC Q94262;  
 DT 01-FEB-1997 (TRENBLREL. 02, Created)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE Hypothetical 50.1 kDa protein.  
 GN K08F11.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 NX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium."  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Murray J., Wohldmann P.,  
 RT "The sequence of C. elegans cosmid K08F11."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Watson R.;  
 RT "Direct Substitution."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U70855; AAB09162.2; -  
 DR HSSP; P00952; 2TSL.  
 DR InterPro; IPR002305; tRNA-synt\_1b.  
 DR InterPro; IPR001412; tRNA-synt\_1.  
 DR InterPro; IPR002307; Tyr tRNA-synt\_1b.  
 DR Pfam; PF00579; tRNA-synt\_1b; 1.  
 DR PRINTS; PRO1040; TRNASYNTTYR.  
 DR TIGRFAMs; TIGR00234; tYRS; 1.  
 DR PROSITE; PS00178; AA\_tRNA\_LIGASE\_I; 1.  
 DR Hypothetical protein.  
 SQ SEQUENCE 447 AA; 50087 MW; 9A085BE761E97DA5 CRC64;  
 Query Match 3.1%; Score 8; DB 5; Length 447;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 103 KAEBLLIL 110  
 Db 289 KAEBLLIL 296

## RESULT 24

063789 PRELIMINARY; PRT; 461 AA.  
 AC 063789;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Phosphatidylinositol 3-kinase regulatory gamma subunit (PI3-kinase  
 DE p55-gamma subunit) (P55PIK) (P55-gamma).  
 GN PI3K3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OK NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MISTER; TISSUE=BRAIN;  
 RX MEDLINE=96214979; PubMed=8621382;  
 RA Inukai K., Anai M., VanBreda E., Hosaka T., Karagiri H., Funaki M.,  
 RA Fukushima Y., Ogihara T., Yazaki Y., Kikuchi M., Oka Y., Asano T.;  
 RT "A novel 55-kDa regulatory subunit for phosphatidylinositol 3-kinase  
 RT structurally similar to p55PIK is generated by alternative splicing of  
 RT the p55alpha gene.";  
 RL J. Biol. Chem. 271:5317-5320 (1996).  
 CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE  
 CC KINASES THROUGH ITS SH2 DOMAIN AND REGULATES THEIR KINASE  
 CC ACTIVITY. DURING INSULIN STIMULATION, IT ALSO BINDS TO IRS-1.  
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P55 (REGULATORY)  
 CC SUBUNITS.  
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND TESTIS. LOWER  
 CC LEVELS IN ADIPOSE TISSUE, KIDNEY, HEART, LUNG AND SKELETAL MUSCLE.  
 CC BARELY DETECTABLE IN LIVER AND SPLEEN.  
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.  
 CC -1- SIMILARITY: HIGH, WITH OTHER P55 SUBUNITS, AND WITH P85-ALPHA AND  
 CC P85-BETA SUBUNITS.  
 DR EMBL: D64047; BAA10927.1; -  
 DR HSPB: P23727; 2PMB  
 DR InterPro: IPR001720; PI3kinase\_P85.  
 DR InterPro: IPR000980; SH2.  
 DR Pfam: PF00017; SH2; 2.  
 DR PRINTS: PR00678; PI3KINASEP85.  
 DR PRODOM: PD000093; SH2; 2.  
 DR SMART: SM00252; SH2; 2.  
 DR PROSITE: PS50001; SH2; 2.  
 DR SH2 domain; Phosphorylation.  
 KW SH2 domain; Phosphorylation.  
 FT DOMAIN 65 163 SH2.  
 FT MODRES 341 341 SH2.  
 SQ SEQUENCE 461 AA; 54254 MW; 6467DB8447CC562B CRC64;  
 Query Match 3.1%; Score 8; DB 11; Length 461;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 116 GAFLRES 123  
 DB 378 GAFLRES 385  
 RESULT 25  
 077132 PRELIMINARY; PRT; 467 AA.  
 AC 077132; Q25195;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Non-receptor protein-tyrosine kinase CSK.  
 GN CSK.  
 OS Hydra attenuata (Hydra) (Hydra vulgaris).  
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;  
 OC Hydrozoa; Hydra.  
 OK NCBI\_TaxID=6067;  
 RN [1]

## RP SEQUENCE FROM N.A.

RC STRAIN=UCI;  
 RX MEDLINE=20408254; PubMed=10951585;  
 RA Miller M.A., Malik I.A., Shenk M.A., Steele R.E.;  
 RT "The Src/Csk regulatory circuit arose early in metazoan evolution.";  
 RT Oncogene 19:3925-3930 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UCI;  
 RA Steele R.E.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL: AF067775; AAC35011.1; -  
 DR HSSP: P41240; 1CSK.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH3; 1.  
 DR PRINTS: PR00401; SH2DOMAIN.  
 DR PRODOM: PD000001; Euk\_pkinase; 1.  
 DR PRODOM: PD000066; SH3; 1.  
 DR PRODOM: PD000093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR SMART: SM00219; TYRK; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE: PS50001; SH2; 1.  
 DR PROSITE: PS50002; SH3; 1.  
 KW ATP-binding; Kinase; Receptor; SH3 domain; Transferase;  
 KW Tyrosine-protein kinase.  
 SQ SEQUENCE 467 AA; 53349 MW; 64A55016B855F2F CRC64;  
 Query Match 3.1%; Score 8; DB 5; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 101 REKAEEL 108  
 DB 99 REKAEEL 106  
 RESULT 26  
 013064 PRELIMINARY; PRT; 488 AA.  
 AC 013064;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Lyn protein tyrosine kinase.  
 GN LYN.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OK NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fukami Y., Funahiki K., Sato K.;  
 RT "Nucleotide sequence of Xenopus Lyn protein tyrosine kinase.";  
 RT Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL: AB003358; BAA20078.1; -  
 DR HSSP: P08631; 1AD5.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.

DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR Prodom; PD000001; Euk\_kinase; 1.  
 DR Prodom; PD000066; SH3; 1.  
 DR Prodom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TyKc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.  
 SQ SEQUENCE 488 AA; 55794 MW; 87E70688BEA92B2 CRC64;

Query Match 3.1%; Score 8; DB 13; Length 488;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLRES 123  
 DB 127 GAFLRES 134

RESULT 27  
 Q94AV6 PRELIMINARY; PRT; 499 AA.  
 AC Q94AV6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE ATG38500/F20M13\_60.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCBT\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,  
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,  
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,  
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinzaki K.,  
 RA Davis R.W., Theologis A., Ecker J.R.,  
 RT "Arabidopsis cDNA clones";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY045693; AAK74051.1;  
 DR InterPro; IPR002198; ADH\_short.  
 DR PROSITE; PS00061; ADH\_SHORT; UNKNOWN 1.  
 SQ SEQUENCE 499 AA; 57761 MW; 878674502EB1B3B CRC64;

Query Match 3.1%; Score 8; DB 10; Length 499;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLVSLR 138  
 DB 8 SLVSLR 15

RESULT 28  
 Q9DDK6 PRELIMINARY; PRT; 502 AA.  
 AC Q9DDK6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Src-family tyrosine kinase SCK.  
 OS Salmo salar (Atlantic salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Plectropterygii; Salmoniformes; Salmonidae; Salmo.  
 NC NCBT\_TaxID=8030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hordvik I., Male R.;  
 RT "A leukocyte cDNA of Atlantic salmon encoding a Src-family tyrosine kinase."  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SMILARTY; CONTAINS 1 SH3 DOMAIN.  
 DR EMBL; AF221110; AAG38611.1; -.  
 DR HSSP; A08631; IAD5.  
 DR InterPro; IPR000719; Euk\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; kinase; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR Prodom; PD000001; Euk\_kinase; 1.  
 DR Prodom; PD000066; SH3; 1.  
 DR Prodom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TyKc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW ATP-binding; Kinase; SH3 domain; Transferase.  
 SQ SEQUENCE 502 AA; 56600 MW; 82DF0D677AA99980 CRC64;

Query Match 3.1%; Score 8; DB 13; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GSYSLVR 135  
 DB 153 GSYSLVR 160

RESULT 29  
 Q62662 PRELIMINARY; PRT; 506 AA.  
 AC Q62662;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Src related tyrosine kinase.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCBT\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 356-416 FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE;  
 RX MEDLINE=94220493; PubMed=8167158;  
 RA Smith I., Avigan M.I.;  
 RT "A newly identified tyrosine kinase is preferentially expressed in the gastrointestinal tract."  
 RL Biochim. Biophys. Acta, Gene Struct. Expr. 1221:348-352 (1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE;  
 RA MEDLINE=9633034; Pubmed=8760296;  
 RX Suntha I.; Avigan M.I.;  
 RT "The apical membranes of mecturing gut columnar epithelial cells  
 RT contain the enzymatically active form of a newly identified fyn-  
 RT related tyrosine kinase.";  
 RL Oncogene 13:547-559(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE;  
 RA Avigan M.I.;  
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL; U09583; AAC52725.1; -.  
 DR HSSP; P00523; 2PTK.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00019; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SMO0252; SH2; 1.  
 DR SMART; SMO0326; SH3; 1.  
 DR SMART; SMO0219; TyKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.  
 SQ SEQUENCE 506 AA; 58166 MW; 69F471DE4F974D82 CRC64;

Query Match 3.1%; Score 8; DB 11; Length 506;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFIRES 123  
 Db 139 GAFIRES 146

RESULT 30  
 ID 061364 PRELIMINARY; PRT; 512 AA.  
 AC 061364;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Protein tyrosine kinase.  
 GN FRK OR BSK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=95137395; Pubmed=7835707;  
 RA Oberg-Welsh C.; Welsh M.; a murine FRK homologue with a specific pattern of  
 RT tissue distribution.";  
 RL Gene 152:239-242(1995).  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL; L36132; AAA65197.1; -.  
 DR HSSP; P00523; 2PTK.  
 DR MGD; MGI:103265; Frk.  
 DR InterPro; IPR000719; Euk\_pkinase.

DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00019; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SMO0252; SH2; 1.  
 DR SMART; SMO0326; SH3; 1.  
 DR SMART; SMO0219; TyKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.  
 SQ SEQUENCE 512 AA; 58892 MW; 4D9DB0AD01997E95 CRC64;

Query Match 3.1%; Score 8; DB 11; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFIRES 123  
 Db 145 GAFIRES 152

RESULT 31  
 ID 061745 PRELIMINARY; PRT; 512 AA.  
 AC 061745;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Intestinal tyrosine kinase.  
 GN FRK OR IYK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=MAMMARY GLAND;  
 RX MEDLINE=95251656; Pubmed=7733928;  
 RA Thiverson M.; Albrecht D.; Zuercher G.; Andres A.; Ziemiecki A.;  
 RT "IYK, a novel intracellular protein tyrosine kinase differentially  
 RT expressed in the mouse mammary gland and intestine.";  
 RL Blochem. Biophys. Res. Commun. 209:582-589(1995).  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL; Z48757; CA88658.1; -.  
 DR HSSP; P00523; 2PTK.  
 DR MGD; MGI:103265; Frk.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00019; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SMO0252; SH2; 1.  
 DR SMART; SMO0326; SH3; 1.  
 DR SMART; SMO0219; TyKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.  
 SQ SEQUENCE 512 AA; 58928 MW; 910D7F27C9BBE3FD CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 8; DB 11; Length 512;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFPIRES 123  
 Db 145 GAFPIRES 152

RESULT 32

0922K9 PRELIMINARY; PRT; 512 AA.

AC 0922K9 01-DEC-2001 (TRENBLREL. 19, Created)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE B-cell src-homology tyrosine kinase.  
 FRK.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Strauberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC007137; AA07137.1; -  
 DR MGD; MGI:103265; Fk.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR01452; SH3.  
 DR InterPro; IPR01245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Pfam; PF00001; Euk\_pkinase; 1.  
 DR Pfam; PF00006; SH3; 1.  
 DR Pfam; PF00009; SH2; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; UNKNOWN\_1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW ATP-binding; Kinase; Transferase.  
 SQ SEQUENCE 512 AA; 58643 MW; 879A0EC07B9EC5F8 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 8; DB 11; Length 512;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFPIRES 123  
 Db 145 GAFPIRES 152

RESULT 33

063206 PRELIMINARY; PRT; 517 AA.

AC 063206 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)  
 DE FGR protein.  
 GN FGR.  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=F344; TISSUE=LEUKEMIA;  
 RA Yue C.C., Labash J.D., Jaye M.;  
 RT "Nucleotide and deduced amino acid sequence of rat FGR.";  
 RL Nucleic Acids Res. 0:0-0(1990).  
 CC 1-SIMILARITY: CONTAINS 1 SH3 DOMAIN.

DR EMBL; X57018; CAA40337.1; -  
 DR HSSP; P00523; 2PTK.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR01452; SH3.  
 DR InterPro; IPR01245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR Prodom; PD000001; Euk\_pkinase; 1.  
 DR Prodom; PD00006; SH2; 1.  
 DR Prodom; PD00009; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW ATP-binding; SH3 domain; Transferase; Tyrosine-protein kinase.  
 SQ SEQUENCE 517 AA; 58792 MW; 852F8F3778C403F CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 8; DB 11; Length 517;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFPIRES 123  
 Db 154 GAFPIRES 161

RESULT 34

08WZK3 PRELIMINARY; PRT; 697 AA.

AC 08WZK3 01-MAR-2002 (TRENBLREL. 20, Created)  
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)  
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)  
 DE Hypothetical 75.6 kDa protein.  
 GN B916.60.

OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariales; Sordariaceae; Neurospora.  
 NX NCBI\_TaxID=5141;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.

RA German Neurospora genome project;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL670003; CAD21241.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 697 AA; 75599 MW; 5371CC36A9657FC9 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 8; DB 3; Length 697;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PPSLSS 19  
|||||  
Db 558 PPSLSS 565

## RESULT 35

ID P87122 PRELIMINARY; PRT; 743 AA.

AC P87122; (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Hypothetical 82.4 kDa protein C3A12.06C in chromosome I.  
GN SPAC3A12.06C.  
OS Schizosaccharomyces pombe (Fission Yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
NCBI\_TaxID=4896;  
RX NCB1\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;  
Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RL -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: SOME, TO C.ELEGANS C07A9.11 AND YEAST YJRI06W.  
DR EMBL; 295395; CAB08751.1; -  
DR InterPro; IPR004837; NaCa\_Ex; 2.  
DR Pfam; PF01699; NaCa\_Ex; 2.

KM Hypothetical protein; Transmembrane.  
FT TRANSMEM 13 33 POTENTIAL.  
FT TRANSMEM 109 129 POTENTIAL.  
FT TRANSMEM 138 158 POTENTIAL.  
FT TRANSMEM 183 203 POTENTIAL.  
FT TRANSMEM 217 237 POTENTIAL.  
FT TRANSMEM 239 259 POTENTIAL.  
FT TRANSMEM 480 500 POTENTIAL.  
FT TRANSMEM 528 548 POTENTIAL.  
FT TRANSMEM 551 571 POTENTIAL.  
FT TRANSMEM 580 600 POTENTIAL.  
FT TRANSMEM 609 629 POTENTIAL.  
FT TRANSMEM 649 669 POTENTIAL.  
FT TRANSMEM 690 710 POTENTIAL.  
FT TRANSMEM 718 738 POTENTIAL.  
SQ SEQUENCE 743 AA; 82396 MW; 15B5FD26FACFB8B8 CRC64;

Query Match 3.1%; Score 8; DB 3; Length 743;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LPSLSS 18  
|||||  
Db 455 LPSLSS 462

## RESULT 36

ID Q9FFK6 PRELIMINARY; PRT; 810 AA.

AC Q9FFK6; (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE Genomic DNA, chromosome 5, pl clone: MJ3.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
NCBI\_TaxID=3702;  
RX NCB1\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=COLUMBIA;

RX MEDLINE=97471969; PubMed=9330910;  
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,  
Miyajima N., Tabata S.;  
RA "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence  
RT features of the 1.6 Mb regions covered by twenty physically assigned  
RT pl clones".  
RL DNA Res. 4:215-230 (1997).  
DR EMBL; AB005237; BAB09662.1; -  
SQ SEQUENCE 810 AA; 89730 MW; 79E20A5E4BDDF069 CRC64;

Query Match 3.1%; Score 8; DB 10; Length 810;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 LSLRGP 58  
|||||  
Db 77 LSLRGP 84

## RESULT 37

ID Q9BL20 PRELIMINARY; PRT; 827 AA.

AC Q9BL20; (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Hypothetical 96.6 kDa protein.  
GN Y488AL.10.  
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Rhabditinae; Caenorhabditis.  
NCBI\_TaxID=6239;  
RX NCB1\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA Waterston R.;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018 (1998).

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Murray J., Du H.;  
RT "The sequence of C. elegans cosmid Y488AL.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Waterston R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC025721; AAK29901.2; -  
KM Hypothetical protein.  
SQ SEQUENCE 827 AA; 96579 MW; 69D297E3446F6C27 CRC64;

Query Match 3.1%; Score 8; DB 5; Length 827;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 ASMDRIRH 147  
|||||  
Db 14 ASMDRIRH 21

## RESULT 38

ID Q9GZT7 PRELIMINARY; PRT; 17 AA.

AC Q9GZT7; (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE OGG1 type 1h (OGG1 type 1d) (Fragment).  
GN OGG1 TYPE 1H OR OGG1 TYPE 1D.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=20184065; PubMed=10717238;  
 RA Shimura K., Kohno T., Takeuchi-Sasaki M., Maeda M., Segawa T.,  
 RA Kamo T., Sugimura H., Yokota J.;  
 RT "Expression of the OGG1-type 1a (nuclear form) protein in cancerous  
 RT and non-cancerous human cells";  
 RL Int. J. Oncol. 16:701-707(2000).  
 DR EMBL; AB037882; BAB13297.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 17 AA; 1748 MW; 824F34170BF91EF CRC64;

Query Match 2.7%; Score 7; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 FPSLOAL 172  
 DB 8 FPSLOAL 14

## RESULT 39

ID Q9HCR6 PRELIMINARY; PRT; 40 AA.  
 AC Q9HCR6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE OGG1 type 1g (fragment).  
 GN OGG1 type 1g.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20184065; PubMed=10717238;  
 RA Shimura K., Kohno T., Takeuchi-Sasaki M., Maeda M., Segawa T.,  
 RA Kamo T., Sugimura H., Yokota J.;  
 RT "Expression of the OGG1-type 1a (nuclear form) protein in cancerous  
 RT and non-cancerous human cells";  
 RL Int. J. Oncol. 16:701-707(2000).  
 DR EMBL; AB037881; BAB13296.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 40 AA; 4380 MW; 4BDB53CAF26C64B3 CRC64;

Query Match 2.7%; Score 7; DB 4; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 FPSLOAL 172  
 DB 8 FPSLOAL 14

## RESULT 40

ID Q9HCR7 PRELIMINARY; PRT; 61 AA.  
 AC Q9HCR7;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE OGG1 type 1f (fragment).  
 GN OGG1 type 1f.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20184065; PubMed=10717238;  
 RA Shimura K., Kohno T., Takeuchi-Sasaki M., Maeda M., Segawa T.,  
 RA Kamo T., Sugimura H., Yokota J.;  
 RT "Expression of the OGG1-type 1a (nuclear form) protein in cancerous  
 RT and non-cancerous human cells";  
 RL Int. J. Oncol. 16:701-707(2000).  
 DR EMBL; AB037880; BAB13295.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 61 AA; 6729 MW; 11CBF729028286F3 CRC64;

Query Match 2.7%; Score 7; DB 4; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 FPSLOAL 172  
 DB 8 FPSLOAL 14

## RESULT 41

ID Q9LWU9 PRELIMINARY; PRT; 70 AA.  
 AC Q9LWU9;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Asparagine synthetase (fragment).  
 GN pPFRU32.  
 OS Pyrus pyrifolia (Japanese pear) (Pyrus serotina).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eusteroideae; Rosales; Rosaceae; Maloideae; Pyrus.  
 OX NCBI\_TaxID=3767;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. KIRUSUI; TISSUE=FRUIT;  
 RA Itai A., Tanaka T., Tanabe K., Tamura F.;  
 RT "Pyrus pyrifolia ripening associated mRNA, clone pPFRU32.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB021793; BAA96452.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 70 AA; 7156 MW; 520F705CA1AE729 CRC64;

Query Match 2.7%; Score 7; DB 10; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ATVALG 41  
 DB 10 ATVALG 16

## RESULT 42

ID Q9PSU0 PRELIMINARY; PRT; 93 AA.  
 AC Q9PSU0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE ZN-MYC oncoprotein (fragment).  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9323639; PubMed=9474440;  
 RA Scheibler-Agus N., Horner J., Torres R., Chiu F.C., Depinho R.A.;  
 RT "Zebra fish myc family and max genes: differential expression and  
 oncogenic activity throughout vertebrate evolution.";

RL Mol. Cell. Biol. 13:2765-2775(1993).  
 DR InterPro: IPR002418; Trp\_Myc.  
 DR Pfam: PF01056; MYC\_N term; 1.  
 SO SEQUENCE 93 AA; 9811 MW; B4409B81CB5BE086 CRC64;

Query Match 2.7%; Score 7; DB 13; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 106 ELLLPFG 112  
 |||||  
 DB 52 ELLLPFG 58

RESULT 43  
 09C7L8 PRELIMINARY; PRT; 96 AA.

AC 09C7L8; 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE Hypothetical 10.5 KDa protein.  
 GN F4C21.32.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 CX NCBI\_TaxId=3702;

RA [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RX MEDLINE=21016719; PubMed=1130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federpiet N.A., Kaul S.,  
 White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brookes S.Y.,  
 Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 Dunn P., Egu P., Feldhym T.V., Feng J.D., Fong B., Fujii C.Y.,  
 Gall J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,  
 Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khatkin B.,  
 Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,  
 Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
 Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 Paig G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 Sun H., Tallon L.J., Tamunga G., Torigai M.O., Town C.D., Walker M.,  
 Uterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,  
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana."  
 RL Nature 408:816-820(2000).  
 DR EMBL: AC069144; AAG51113.1; -  
 KW Hypothetical protein  
 SO SEQUENCE 96 AA; 10525 MW; 75BC651B29468A39 CRC64;

Query Match 2.7%; Score 7; DB 10; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 168 SLOALVD 174  
 |||||  
 DB 62 SLOALVD 68

RESULT 44  
 08WUD9 PRELIMINARY; PRT; 102 AA.

AC 08WUD9; 01-MAR-2002 (TREMblrel. 20, Created)  
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Similar to RIKEN cDNA 1200014N16 gene.  
 SO Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxId=9606;

RA [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TESTIS;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC020784; AAH20784.1; -  
 SO SEQUENCE 102 AA; 10778 MW; 18C9E173F4FB939D CRC64;

Query Match 2.7%; Score 7; DB 4; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 192 VLQRAFP 198  
 |||||  
 DB 40 VLQRAFP 46

RESULT 45  
 05S970 PRELIMINARY; PRT; 106 AA.

AC 05S970; 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Hypothetical protein 8110669.  
 GN SL00669.  
 OS Synchocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.  
 CX NCBI\_TaxId=1148;

RA [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96127529; PubMed=8590279;  
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Suzuki T., Miyajima N.,  
 Sugiura M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 region from map positions 64% to 92% of the genome."  
 RL DNA Res. 2:153-166(1995).  
 RN [2]

RA [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asanizu E., Nakamura Y.,  
 Miyajima N., Hikosawa M., Sugiura M., Sasamoto S., Kimura T.,  
 Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,  
 Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synchocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions."  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL: D64005; BBA10747.1; -  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 106 AA; 12351 MW; 7FEB1C429C82493 CRC64;

Query Match 2.7%; Score 7; DB 16; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 SPSSSS 19  
 |||||  
 DB 85 SPSSSS 91

RESULT 46  
 09D4J0 PRELIMINARY; PRT; 109 AA.

AC 09D4J0; 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)



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DE 4931430N09R1k protein.
GN 4931430N09R1k.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.W., Staudt P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Ohtdo T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guecinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Montheres P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL/ AK016492: BAB30269.1; -
DR MGD; MGI:1921613: 4931430N09R1k.
SQ SEQUENCE 109 AA; 13056 MW; A155B018F113E92 CRC64;

Query Match 2.7%; Score 7; DB 11; Length 109;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 LYEGLSR 101
DB 74 LYEGLSR 80

RESULT 47
Q95572 PRELIMINARY; PRT; 114 AA.
AC Q95572;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PA0624.
GN PA0624.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RA Nakayama K., Takashima K., Ishihara H., Shiomura T., Kageyama M.,
RA Kanaya S., Ohnishi M., Murata T., Terawaki T., Mori H., Hayashi T.;
RT "Genetic relationship between bacteriophages and bacteriophages.";
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RA MEDLINE=20437337; PubMed=1098403;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey W.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wagner S., Yuan Y.,
RA Brody L.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lam R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Retzer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;

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RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL/ AB030825; BAA83162.1; -
DR EMBL/ AE004498; AAG04013.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 114 AA; 12523 MW; 3C22EE61270EF50D CRC64;

Query Match 2.7%; Score 7; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 VRLSRPA 140
DB 20 VRLSRPA 26

RESULT 48
Q8Y8W4 PRELIMINARY; PRT; 115 AA.
AC Q8Y8W4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein lmo0778.
GN lmo0778.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BGD-E / SEROVAR 1/2a;
RA MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Cheuani F., Couve E., de Darvar A., Deloux P.,
RA Domani E., Dominguez-Bernal G., Duchud E., Durant L., Dussauget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf U., Jackson D.,
RA Jones L.-W., Kaerst U., Kreft U., Kunz M., Kunz F., Kurpkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjati H.,
RA Nordstedt G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL/ AL591976; CAC98856.1; -
DR Listeriac; LMO00778; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 115 AA; 13596 MW; 5414CD46FD07531 CRC64;

Query Match 2.7%; Score 7; DB 16; Length 115;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 RIRHYRI 150
DB 64 RIRHYRI 70

RESULT 49
Q9UFL7 PRELIMINARY; PRT; 117 AA.
AC Q9UFL7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Hypothetical 12.7 kDa protein.
GN DKFZP434K058.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TESTIS;  
 RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL117583; CAB56005.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 117 AA; 12742 MW; 582E52156AE7BD29 CRC64;

Query Match 2.7%; Score 7; DB 4; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 81;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 164 LTRPSIQ 170  
 |||||  
 Db 34 LTRPSIQ 40

## RESULT 50

092FH6 PRELIMINARY; PRT; 118 AA.  
 AC 092FH6;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein lin0130.  
 GN LIN0130.  
 OS Listeria innocua.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Listeriaceae; Listeria.  
 OX NCBI\_TaxID=1642;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CLIP 11262 / SEROVAR 6A;  
 RX PubMed=11679669;  
 RA Glasner P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,  
 Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,  
 Demain E., Dominguez-Bernal G., Duchaud E., Durant L., Duseurget O.,  
 Entian K.-D., Eslin H., Garcia-del Portillo F., Garrido P.,  
 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
 Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkut G.,  
 Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,  
 Nordiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,  
 Rammel B., Rose M., Schueter T., Simoes N., Tierrez A.,  
 Vazquez-Boland J.-A., Voas H., Weiland J., Cosset P.;  
 RT "Comparative genomics of Listeria species.";  
 RL Science 294:849-852(2001).  
 DR EMBL; AU596163; CAC95363.1; -;  
 DR ListList; LIN00130; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 118 AA; 13930 MW; 9118528B7C1FA5 CRC64;

Query Match 2.7%; Score 7; DB 16; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 81;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 144 RIRHYRI 150  
 |||||  
 Db 65 RIRHYRI 71

Search completed: March 24, 2003, 16:08:06  
 Job time : 44 secs